5_3_Magic_BLAST_contigs_specific

July 25, 2021

Summary of magicblast

[1]:
```
import numpy as np
import os.path
import pandas as pd
from matplotlib import pyplot as plt
import seaborn as sns
from pandas.plotting import scatter_matrix
import pathlib
import warnings
warnings.filterwarnings('ignore')
```

[2]:
```
from IPython.core.display import display, HTML
display(HTML("<style>.container { width:95% !important; }</style>"))
```

```
<IPython.core.display.HTML object>
```

[3]:
```
PROJECT_CODE='PRJNA606875'
BASE_PATH = f'/mnt/1TB_0/Data/Assembly/{PROJECT_CODE}/'

dbname='nt'
kmer='k141'
kmer_extra='k29'

#magicblast on contigs
magic_blast_sam_tail=f'_{dbname}_final_contigs_magicBLAST.sam'
f_contigs_file_tail=f'_{dbname}_magic_blast_asc_contigs.txt'
GIS,ACCESSIONS,TITLES=None,None,None
```

0.0.1 All SRA's

[4]:
```
sra_list=['SRR11093265',␣
↪'SRR11093266','SRR11093267','SRR11093268','SRR11093269','SRR11093270','SRR11093271']
```

[5]:
```
def read_gi_accession_title(gi_asc_file):
    gis=[]
    accessions=[]
    titles=[]
    with open(gi_asc_file, 'r') as infile:
        data = infile.readlines()
        for i in data:
            output=i.split(' ',2)
            gis.append(output[0])
            accessions.append(output[1])
            titles.append(output[2])
    return gis, accessions, titles
```

[6]:
```
def set_accessions():
    global GIS
    global ACCESSIONS
    global TITLES
    GIS,ACCESSIONS,TITLES=read_gi_accession_title('/mnt/1TB_ssd/Data/BLAST/nt.
 ↪gi_taxid.tsv')
```

0.0.2 Stats

[7]:
```
def get_asc_descr_count(sra):
    accessions=[]
    descriptions=[]
    counts=[]
    path = BASE_PATH+sra+'/magic_blast/'
    f_mer=path+f'{sra}_{dbname}_{kmer}_magicBLAST_summary.txt'
    if not os.path.isfile(f_mer):
        f_mer=path+f'{sra}_{dbname}_{kmer_extra}_magicBLAST_summary.txt'
    assert os.path.isfile(f_mer)
    with open(f_mer, 'r') as f:
        lines = [line.rstrip('\n') for line in f]
        total=len(lines)-1
        for line in lines:
            if not 'database:' in line: #ignore header
                asc=line.split(None, 1)[0]
                title=line.split(None, 1)[1].split(', count:')[0]
                count=line.split(None, 1)[1].split(', count:')[1]
                accessions.append(asc)
                descriptions.append(title)
                counts.append(int(count))
    return accessions, descriptions, counts, total
```

[8]:
```
def get_indexes(substr, str_list):
    index_list = []
    i = 0
    for e in str_list:
        if substr in e.lower():
            index_list.append(i)
        i +=1
    return index_list
```

```
[9]: for i,sra in enumerate(sra_list):
         accessions, descriptions, counts, total=get_asc_descr_count(sra)
         print(f'{sra}, matched contigs: {sum(counts)}')
```

```
SRR11093265, matched contigs: 44
SRR11093266, matched contigs: 549
SRR11093267, matched contigs: 2056
SRR11093268, matched contigs: 189
SRR11093269, matched contigs: 1698
SRR11093270, matched contigs: 19067
SRR11093271, matched contigs: 156
```

```
[10]: def get_desc_count(qstring, descriptions, counts, lowercase=True):
          qd=[]
          qc=0
          for d,c in zip(descriptions, counts):
              if lowercase:
                  if qstring.lower() in d.lower():
                      qd.append(d)
                      qc=qc+int(c)
              else:
                  if qstring in d:
                      qd.append(d)
                      qc=qc+int(c)
          return qd, qc
```

```
[11]: def get_descr(sra):
          accessions, descriptions, counts, total=get_asc_descr_count(sra)
          print(f'sra: {sra}, accessions: {len(accessions)}, descriptions:␣
       ↪{len(descriptions)}, counts: {len(counts)}, total: {total}')
          if total>0:
              human,humanc = get_desc_count('human', descriptions, counts)
              homo_sapiens,homo_sapiensc = get_desc_count('homo sapiens',␣
       ↪descriptions, counts)
              h_sapiens,h_sapiensc = get_desc_count('h.sapiens', descriptions, counts)
              human_contigs = human+homo_sapiens+h_sapiens
              human_counts = humanc+homo_sapiensc+h_sapiensc
              pangolin, pangolinc = get_desc_count('manis javanica', descriptions,␣
       ↪counts)
              pangolin_p, pangolin_pc = get_desc_count('manis pentadactyla',␣
       ↪descriptions, counts)
              pangolin=pangolin+pangolin_p
              pangolin_counts=pangolinc+pangolin_pc
              mouse,mousec = get_desc_count('mus musculus', descriptions, counts)
```

```
        vector,vectorc= get_desc_count('vector', descriptions, counts)
        pig,pigc = get_desc_count('sus scrofa', descriptions, counts)
        cat,catc = get_desc_count('felis catus', descriptions, counts)
        tiger,tigerc = get_desc_count('panthera tigris', descriptions, counts)
        dog,dogc = get_desc_count('canis lupus', descriptions, counts)
        virus,virusc = get_desc_count('virus', descriptions, counts)

        mulatta,mulattac = get_desc_count('mulatta', descriptions, counts)
        troglodytes,troglodytesc = get_desc_count('troglodytes', descriptions,␣
↪counts)
        pongo,pongoc =get_desc_count('pongo', descriptions, counts)
        papio,papioc = get_desc_count('papio', descriptions, counts)
        mandrillus,mandrillusc =get_desc_count('mandrillus', descriptions,␣
↪counts)
        cercocebus,cercocebusc =get_desc_count('cercocebus', descriptions,␣
↪counts)
        gelada,geladac =get_desc_count('gelada', descriptions, counts)
        monkey = mulatta+troglodytes+pongo+papio+mandrillus+cercocebus+gelada
        monkey_counts =␣
↪mulattac+troglodytesc+pongoc+papioc+mandrillusc+cercocebusc+geladac

        mustela,mustelac= get_desc_count('mustela', descriptions, counts)

        pipistrellus,pipistrellusc =get_desc_count('pipistrellus',␣
↪descriptions, counts)
        rhinolophus,rhinolophusc = get_desc_count('rhinolophus', descriptions,␣
↪counts)
        pteropus,pteropusc = get_desc_count('pteropus', descriptions, counts)
        myotis,myotisc = get_desc_count('myotis', descriptions, counts)
        bat = pipistrellus + rhinolophus+pteropus+myotis
        bat_counts = pipistrellusc + rhinolophusc+pteropusc+myotisc

        mycoplasma,mycoplasmac = get_desc_count('mycoplasma', descriptions,␣
↪counts)

        lst = ['human', 'monkey', 'pangolin', 'mouse',
                'pig', 'cat', 'tiger', 'dog', 'bat', 'virus',␣
↪'vector','mycoplasma','mustela']
        lengths = [human_counts, monkey_counts, pangolin_counts, mousec,
                pigc, catc, tigerc, dogc, bat_counts, virusc, vectorc,␣
↪mycoplasmac,mustelac]
        final_contigs=BASE_PATH+sra+'/megahit_default/final.contigs.fa'
        with open(final_contigs) as final_contigs_file:
            total_contigs=sum(1 for _ in final_contigs_file)
        res = [int(i) for i in counts]
        total_contigs_matched=sum(res)
        sra_l=[sra]*len(lst)
        fractions_matched = [human_counts/total_contigs_matched, monkey_counts/
↪total_contigs_matched, pangolin_counts/total_contigs_matched, mousec/
↪total_contigs_matched,
                pigc/total_contigs_matched, catc/total_contigs_matched, tigerc/
↪total_contigs_matched, dogc/total_contigs_matched, bat_counts/
↪total_contigs_matched,
                             virusc/total_contigs_matched, vectorc/
↪total_contigs_matched, mycoplasmac/total_contigs_matched, mustelac/
↪total_contigs_matched]
        pct_matched = [round(i * 100,2) for i in fractions_matched]
        df = pd.DataFrame(list(zip(sra_l, lst, lengths, pct_matched)),
                   columns =['SRA','Name', 'count', 'pct_matched'])
        return df
    return None
```

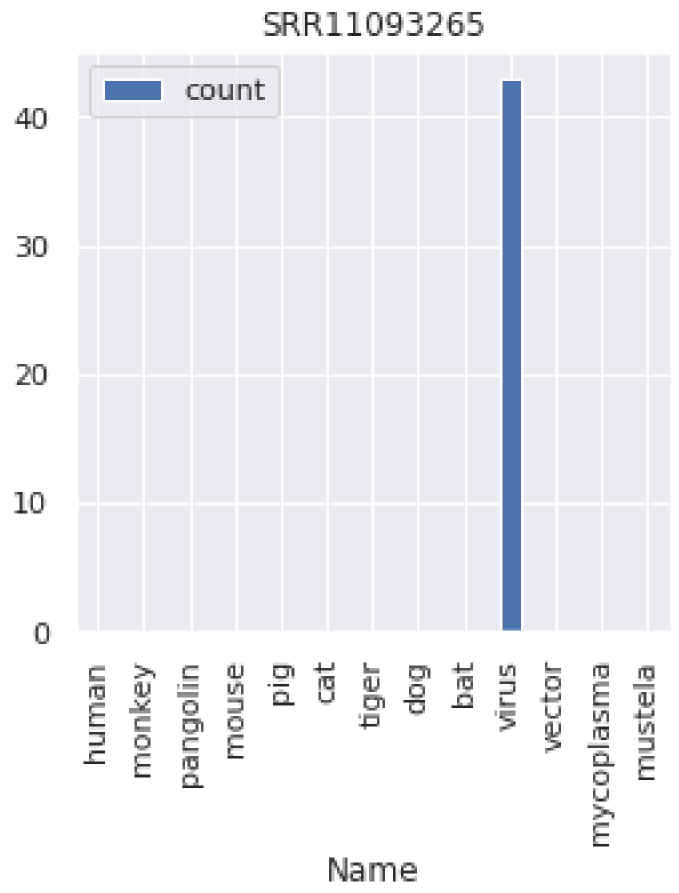
[12]:
```
sns.set(rc={"figure.figsize":(4, 4)})
def plot_df(df, sra):
    ax=df.plot(x='Name', y='count', kind='bar')
    ax.set_title(sra, fontsize=12)
    #ax.set_yscale('log')
    #ax.set_ylim([0,df['count'].max()+10])
    ax.set_ylim(bottom=0)
    fig = plt.gcf()
    fig.savefig(BASE_PATH+sra+'/magic_blast/
↪'+f'{sra}_{dbname}_{kmer}_magicBLAST_species.png', bbox_inches="tight")
```

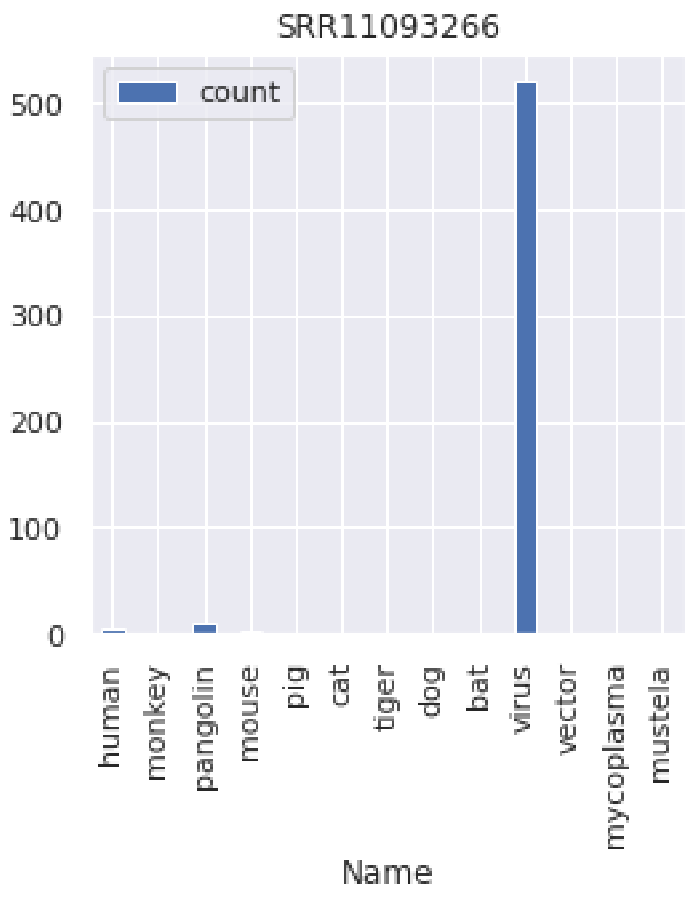
[13]:
```
for sra in sra_list:
    print(sra)
    try:
        df=get_descr(sra)
        print(df.head())
        df.to_csv(BASE_PATH+sra+'/magic_blast/
↪'+f'{sra}_{dbname}_{kmer}_magicBLAST_species_df.csv')
        plot_df(df, sra)
    except FileNotFoundError:
        print(e)
        pass
    except AttributeError:
        pass
```

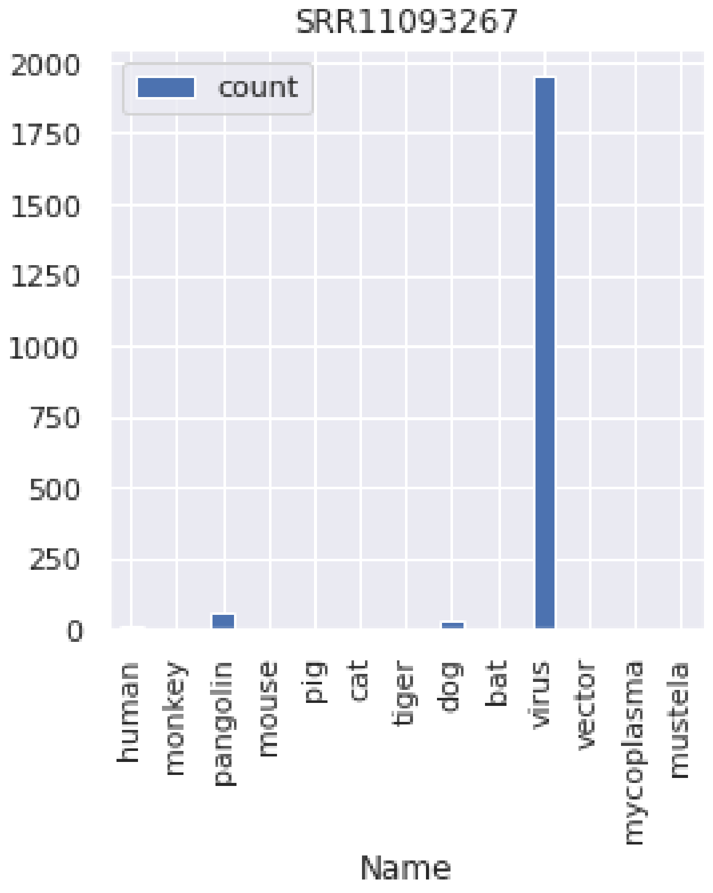
```
SRR11093265
sra: SRR11093265, accessions: 10, descriptions: 10, counts: 10, total: 10
           SRA      Name  count  pct_matched
0  SRR11093265     human      0          0.0
1  SRR11093265    monkey      0          0.0
2  SRR11093265  pangolin      0          0.0
```

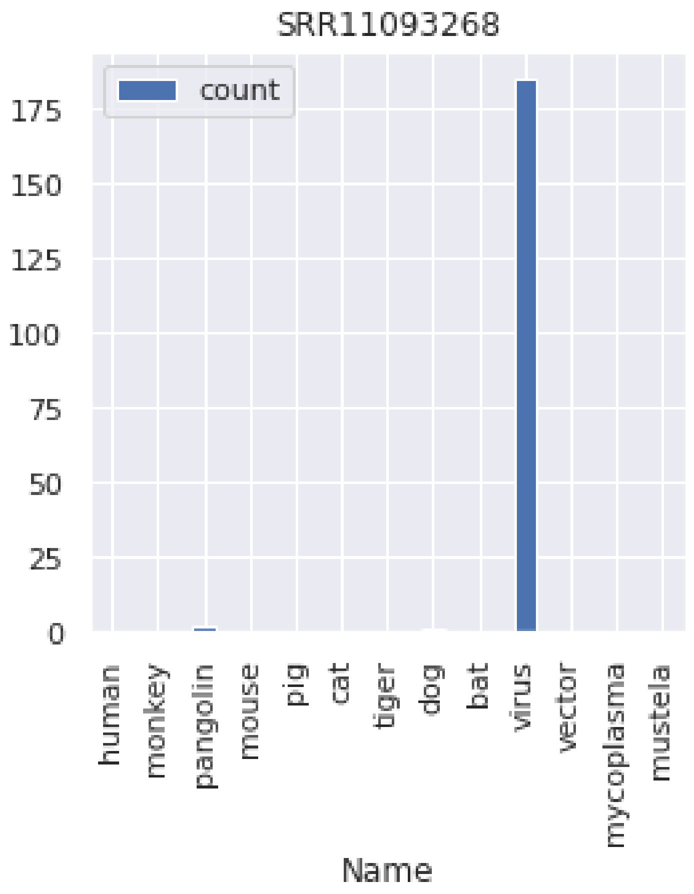
```
3  SRR11093265     mouse      0          0.0
4  SRR11093265       pig      0          0.0
SRR11093266
sra: SRR11093266, accessions: 34, descriptions: 34, counts: 34, total: 34
           SRA      Name  count  pct_matched
0  SRR11093266     human      6         1.09
1  SRR11093266    monkey      0         0.00
2  SRR11093266  pangolin     10         1.82
3  SRR11093266     mouse      2         0.36
4  SRR11093266       pig      0         0.00
SRR11093267
sra: SRR11093267, accessions: 100, descriptions: 100, counts: 100, total: 100
           SRA      Name  count  pct_matched
0  SRR11093267     human      6         0.29
1  SRR11093267    monkey      4         0.19
2  SRR11093267  pangolin     57         2.77
3  SRR11093267     mouse      0         0.00
4  SRR11093267       pig      0         0.00
SRR11093268
sra: SRR11093268, accessions: 10, descriptions: 10, counts: 10, total: 10
           SRA      Name  count  pct_matched
0  SRR11093268     human      0         0.00
1  SRR11093268    monkey      0         0.00
2  SRR11093268  pangolin      2         1.06
3  SRR11093268     mouse      0         0.00
4  SRR11093268       pig      0         0.00
SRR11093269
sra: SRR11093269, accessions: 223, descriptions: 223, counts: 223, total: 223
           SRA      Name  count  pct_matched
0  SRR11093269     human     13         0.77
1  SRR11093269    monkey      2         0.12
2  SRR11093269  pangolin    160         9.42
3  SRR11093269     mouse      2         0.12
4  SRR11093269       pig      1         0.06
SRR11093270
sra: SRR11093270, accessions: 11832, descriptions: 11832, counts: 11832, total:
11832
           SRA      Name  count  pct_matched
0  SRR11093270     human    110         0.58
1  SRR11093270    monkey     13         0.07
2  SRR11093270  pangolin  18413        96.57
3  SRR11093270     mouse     26         0.14
4  SRR11093270       pig     14         0.07
SRR11093271
sra: SRR11093271, accessions: 74, descriptions: 74, counts: 74, total: 74
           SRA      Name  count  pct_matched
0  SRR11093271     human      4         2.56
1  SRR11093271    monkey     22        14.10
```

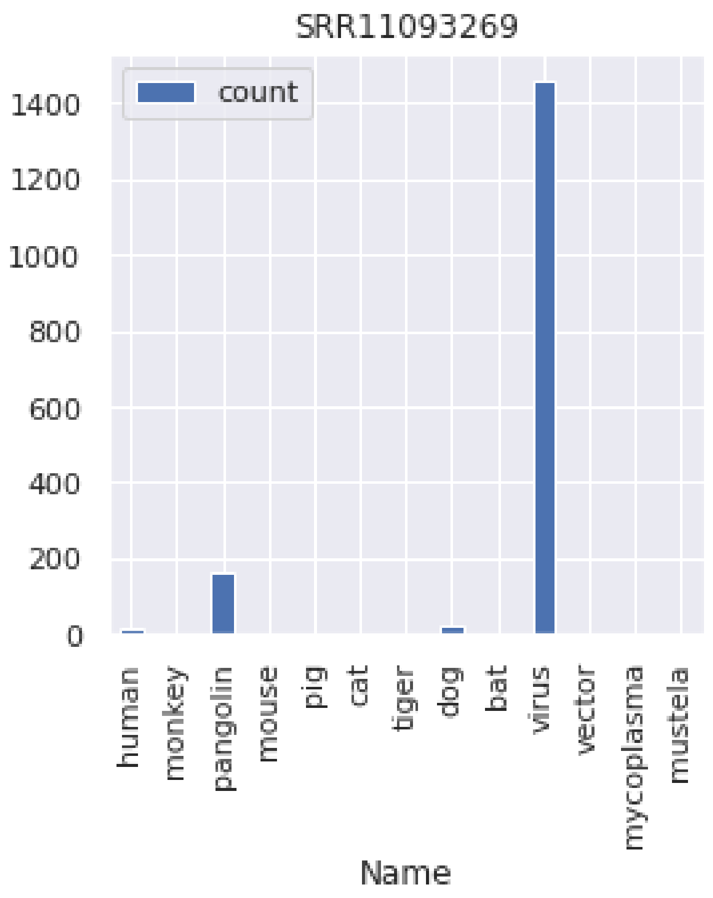
```
2  SRR11093271  pangolin      0         0.00
3  SRR11093271     mouse      0         0.00
4  SRR11093271       pig      0         0.00
```

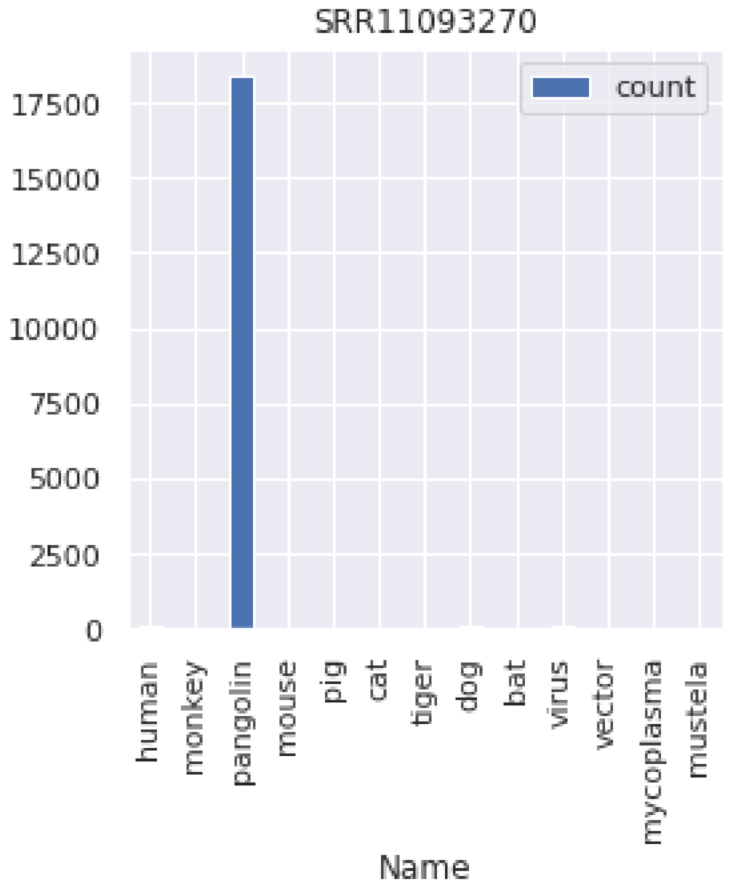


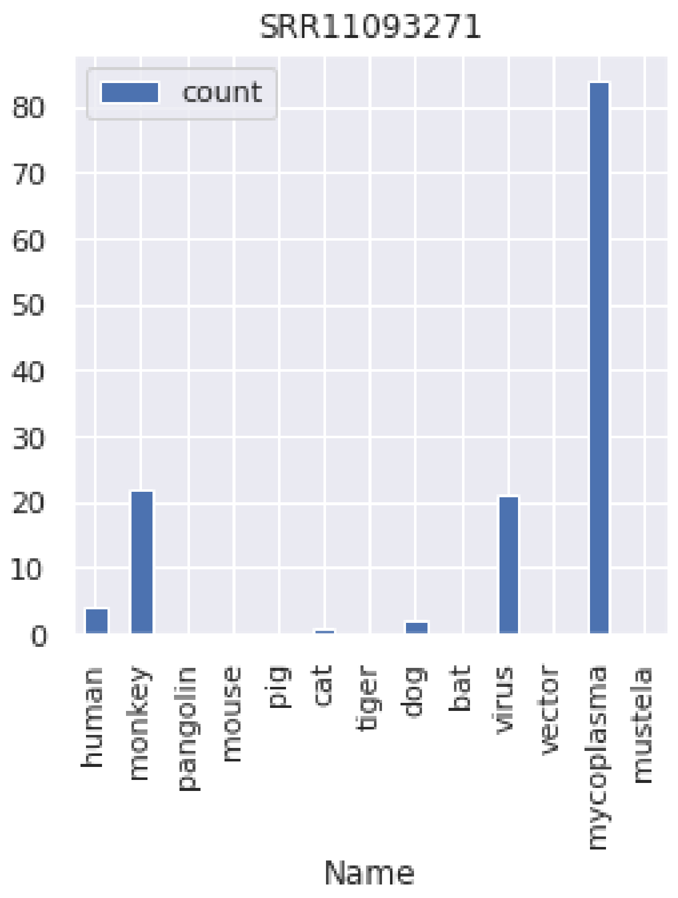

SRR11093266
count
500
400
300
200
100
0
human
monkey
pangolin
mouse
pig
cat
tiger
dog
bat
virus
vector
mycoplasma
mustela
Name


SRR11093267
count
2000
1750
1500
1250
1000
750
500
250
0
human
monkey
pangolin
mouse
pig
cat
tiger
dog
bat
virus
vector
mycoplasma
mustela
Name


SRR11093268
count
175
150
125
100
75
50
25
0
human
monkey
pangolin
mouse
pig
cat
tiger
dog
bat
virus
vector
mycoplasma
mustela
Name


SRR11093269
count
1400
1200
1000
800
600
400
200
0
human
monkey
pangolin
mouse
pig
cat
tiger
dog
bat
virus
vector
mycoplasma
mustela
Name


SRR11093270
count
17500
15000
12500
10000
7500
5000
2500
0
human
monkey
pangolin
mouse
pig
cat
tiger
dog
bat
virus
vector
mycoplasma
mustela
Name

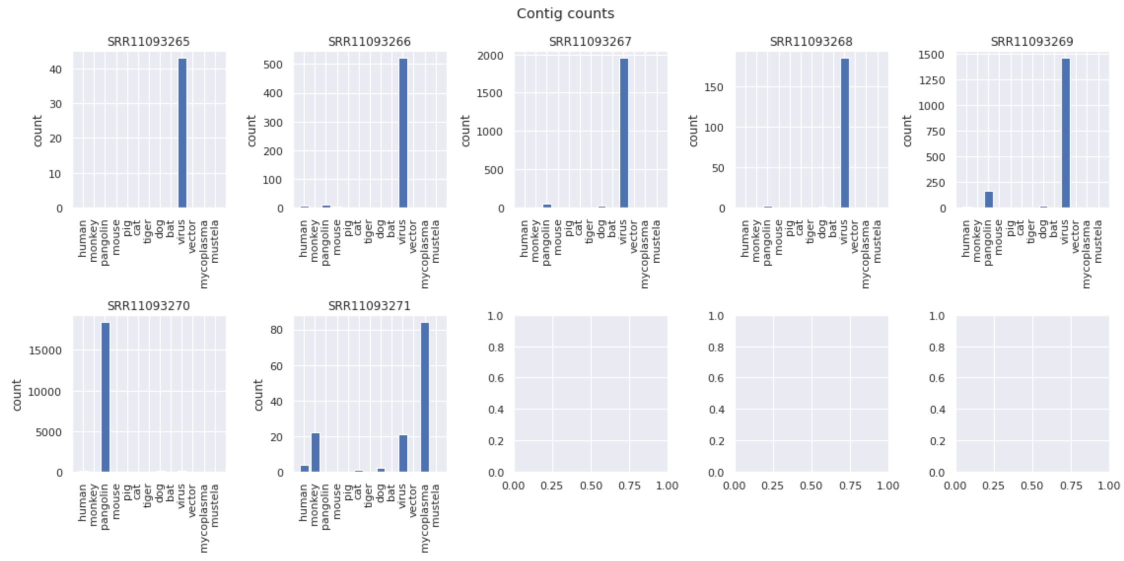


```
[14]: pathlib.Path(BASE_PATH+'general_plots/').mkdir(exist_ok=True)

      def multi_plot():
          fig, axis = plt.subplots(2, 5,figsize=(16,8))
          fig.suptitle('Contig counts')
          sra=sra_list[0]
          df=get_descr(sra)
          axis[0,0].bar(df['Name'],df['count'])
          axis[0,0].tick_params(axis='x', rotation=90)
          axis[0,0].set_ylabel('count')
          axis[0,0].title.set_text(sra)

          sra=sra_list[1]
          df=get_descr(sra)
          axis[0,1].bar(df['Name'],df['count'])
          axis[0,1].set_ylabel('count')
          axis[0,1].tick_params(axis='x', rotation=90)
          axis[0,1].set_ylabel('count')
          axis[0,1].title.set_text(sra)
```

```
    sra=sra_list[2]
    df=get_descr(sra)
    axis[0,2].bar(df['Name'],df['count'])
    axis[0,2].set_ylabel('count')
    axis[0,2].tick_params(axis='x', rotation=90)
    axis[0,2].set_ylabel('count')
    axis[0,2].title.set_text(sra)

    sra=sra_list[3]
    df=get_descr(sra)
    axis[0,3].bar(df['Name'],df['count'])
    axis[0,3].set_ylabel('count')
    axis[0,3].tick_params(axis='x', rotation=90)
    axis[0,3].set_ylabel('count')
    axis[0,3].title.set_text(sra)

    sra=sra_list[4]
    df=get_descr(sra)
    axis[0,4].bar(df['Name'],df['count'])
    axis[0,4].set_ylabel('count')
    axis[0,4].tick_params(axis='x', rotation=90)
    axis[0,4].set_ylabel('count')
    axis[0,4].title.set_text(sra)


    sra=sra_list[5]
    df=get_descr(sra)
    axis[1,0].bar(df['Name'],df['count'])
    axis[1,0].set_ylabel('count')
    axis[1,0].tick_params(axis='x', rotation=90)
    axis[1,0].set_ylabel('count')
    axis[1,0].title.set_text(sra)

    sra=sra_list[6]
    df=get_descr(sra)
    axis[1,1].bar(df['Name'],df['count'])
    axis[1,1].set_ylabel('count')
    axis[1,1].tick_params(axis='x', rotation=90)
    axis[1,1].set_ylabel('count')
    axis[1,1].title.set_text(sra)

    fig.tight_layout()
    fig.savefig(BASE_PATH+'general_plots/
↪'+f'{sra}_{dbname}_{kmer}_magicBLAST_contig_count_matrix.png',␣
↪bbox_inches="tight")
    plt.show()
```

```
[15]: multi_plot()
```

```
sra: SRR11093265, accessions: 10, descriptions: 10, counts: 10, total: 10
sra: SRR11093266, accessions: 34, descriptions: 34, counts: 34, total: 34
sra: SRR11093267, accessions: 100, descriptions: 100, counts: 100, total: 100
sra: SRR11093268, accessions: 10, descriptions: 10, counts: 10, total: 10
sra: SRR11093269, accessions: 223, descriptions: 223, counts: 223, total: 223
sra: SRR11093270, accessions: 11832, descriptions: 11832, counts: 11832, total:
11832
sra: SRR11093271, accessions: 74, descriptions: 74, counts: 74, total: 74
```



```
[16]: frames=[]
      for i,sra in enumerate(sra_list):
          try:
              df = pd.read_csv(BASE_PATH+sra+'/magic_blast/
       ↪'+f'{sra}_{dbname}_{kmer}_magicBLAST_species_df.csv')
              x = df.Name.astype('category')
              df['species_uid'] =x.cat.codes
              df['SRA_val'] =df.SRA.str.strip('SRR')
              df['SRA_val'] = pd.to_numeric(df['SRA_val'])
              frames.append(df)
          except FileNotFoundError:
              pass
      df_sra = pd.concat(frames)
```

```
[17]: df_sra.drop(columns=['Unnamed: 0'],inplace=True)
```

[18]:
```
df_sra.head(n=10)
```

[18]:
```
           SRA      Name  count  pct_matched  species_uid    SRA_val
0  SRR11093265     human      0         0.00            3  11093265
1  SRR11093265    monkey      0         0.00            4  11093265
2  SRR11093265  pangolin      0         0.00            8  11093265
3  SRR11093265     mouse      0         0.00            5  11093265
4  SRR11093265       pig      0         0.00            9  11093265
5  SRR11093265       cat      0         0.00            1  11093265
6  SRR11093265     tiger      0         0.00           10  11093265
7  SRR11093265       dog      0         0.00            2  11093265
8  SRR11093265       bat      0         0.00            0  11093265
9  SRR11093265     virus     43        97.73           12  11093265
```

[19]:
```
df_sra.Name.unique()
```

[19]:
```
array(['human', 'monkey', 'pangolin', 'mouse', 'pig', 'cat', 'tiger',
       'dog', 'bat', 'virus', 'vector', 'mycoplasma', 'mustela'],
      dtype=object)
```

0.0.3 All nt database matches

[20]:
```
total_dict={}
asc_desc={}
for sra in sra_list:
    accessions, descriptions, counts, total=get_asc_descr_count(sra)
    for asc,desc,cnt in zip(accessions,descriptions, counts):
        if asc in total_dict:
            total_dict[asc]+=int(cnt)
        else:
            total_dict[asc]=int(cnt)
        if asc not in asc_desc:
            asc_desc[asc]=desc
```

[21]:
```
assert len(total_dict)==len(asc_desc)
```

[22]:
```
len(asc_desc)
```

[22]:
```
12158
```

Print out the 100 most common nt database classification for all contigs in the project

[23]:
```
def print_top_n_sp(total_dict, max_num):
    listofTuples = sorted(total_dict.items() , reverse=True, key=lambda x: x[1])
    for i, elem in enumerate(listofTuples):
        if i<max_num:
            print(asc_desc[elem[0]], ": " , elem[1] )
        else:
            break
```

[24]:
```
print_top_n_sp(total_dict, max_num=10)
```

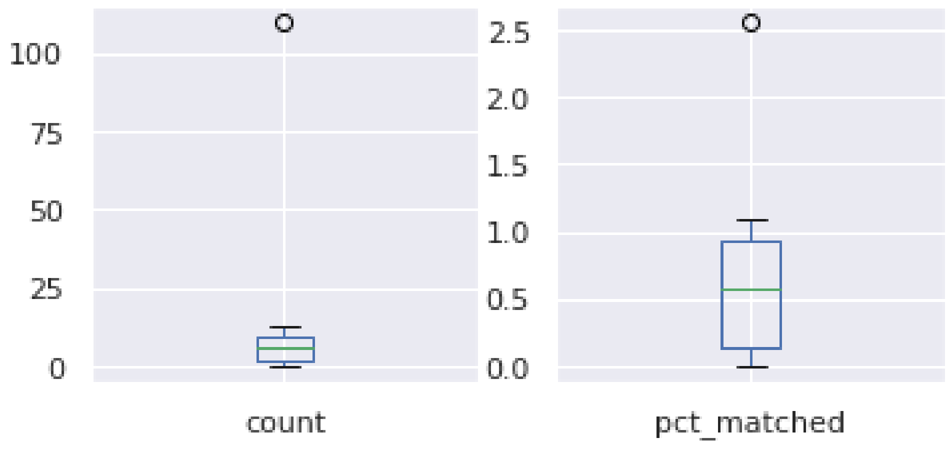
```
Pangolin coronavirus isolate PCoV_GX-P5L, complete genome :  837
Pangolin coronavirus isolate PCoV_GX-P1E, complete genome :  787
Pangolin coronavirus isolate PCoV_GX-P2V, complete genome :  756
Pangolin coronavirus isolate PCoV_GX-P4L, complete genome :  715
Pangolin coronavirus isolate PCoV_GX-P5E, complete genome :  641
Pangolin coronavirus isolate PCoV_GX-P3B genomic sequence :  478
PREDICTED: Manis javanica proline rich coiled-coil 2A (PRRC2A), mRNA :  15
Pangolin coronavirus isolate MP789, complete genome :  14
Manis javanica isolate MP_PG03-UM mitochondrion, complete genome :  14
PREDICTED: Manis javanica LDL receptor related protein 1 (LRP1), transcript
variant X3, mRNA :  14
```

0.0.4 Human

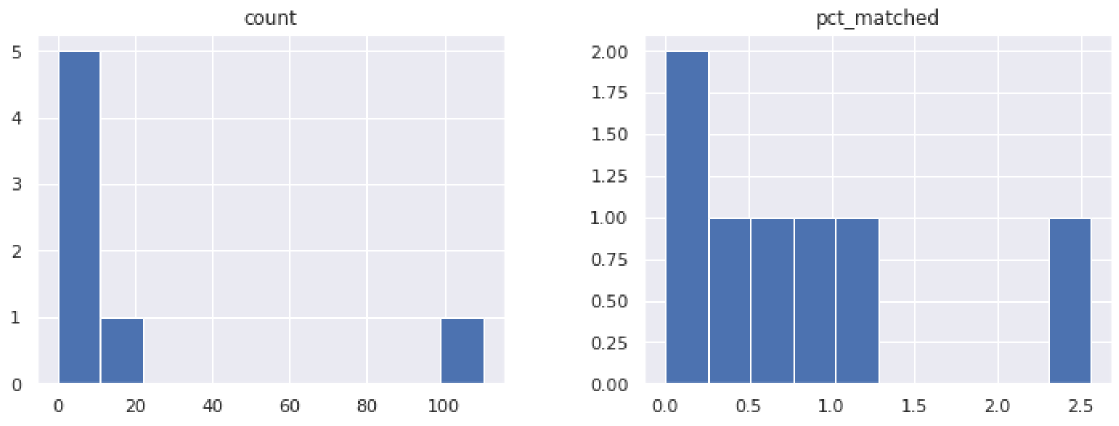
[25]:
```
df=df_sra[df_sra['Name'].str.contains('human')]
```

[26]:
```
df.drop(columns=['Name'],inplace=True)
sns.set(rc={"figure.figsize":(6, 6)})
df_box=df[['count', 'pct_matched']]
df_box.plot(kind='box', subplots=True, layout=(4,4), sharex=False,␣
 ↪sharey=False, figsize=(12,12))
```

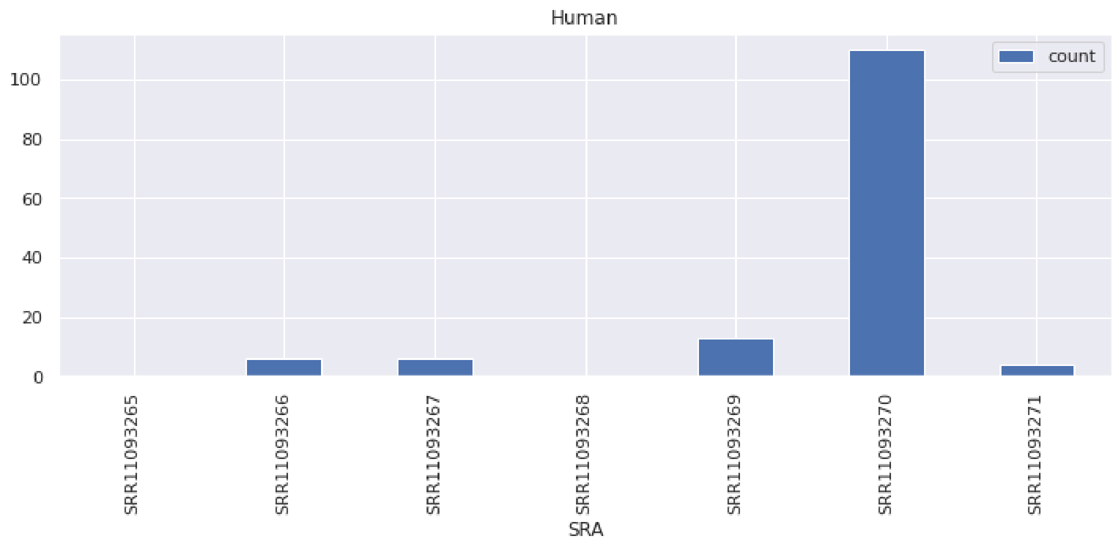
[26]:
```
count             AxesSubplot(0.125,0.71587;0.168478x0.16413)
pct_matched    AxesSubplot(0.327174,0.71587;0.168478x0.16413)
dtype: object
```



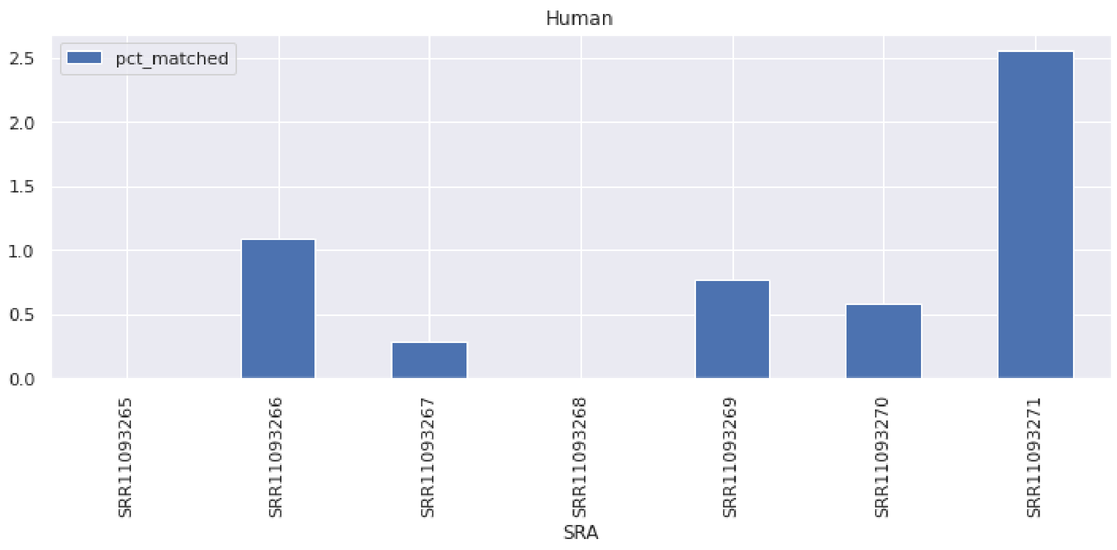
[27]:
```
df_box.hist(figsize=(12,4))
plt.show()
```



[28]:
```
ax=df.plot(x='SRA', y='count', kind='bar',figsize=(12,4))
ax.set_title('Human', fontsize=12)
plt.show()
```



[29]:
```
ax=df.plot(x='SRA', y='pct_matched', kind='bar',figsize=(12,4))
ax.set_title('Human', fontsize=12)
plt.show()
```



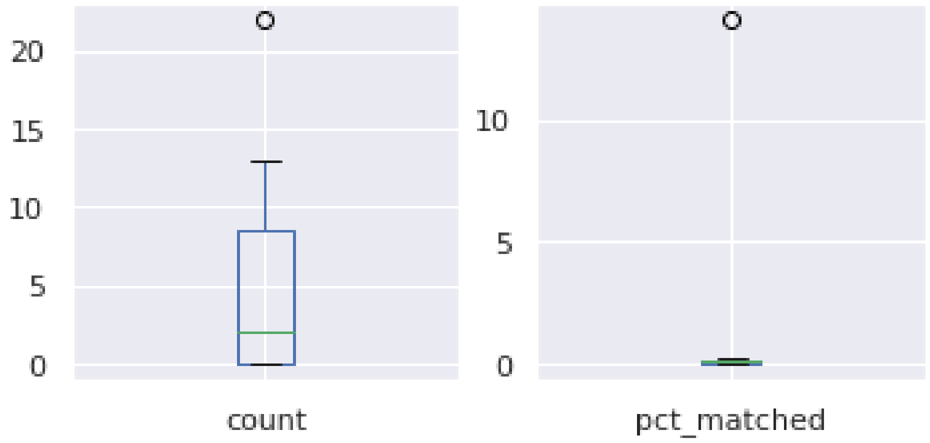
0.0.5 Monkey

[30]:
```python
s_name='monkey'
```

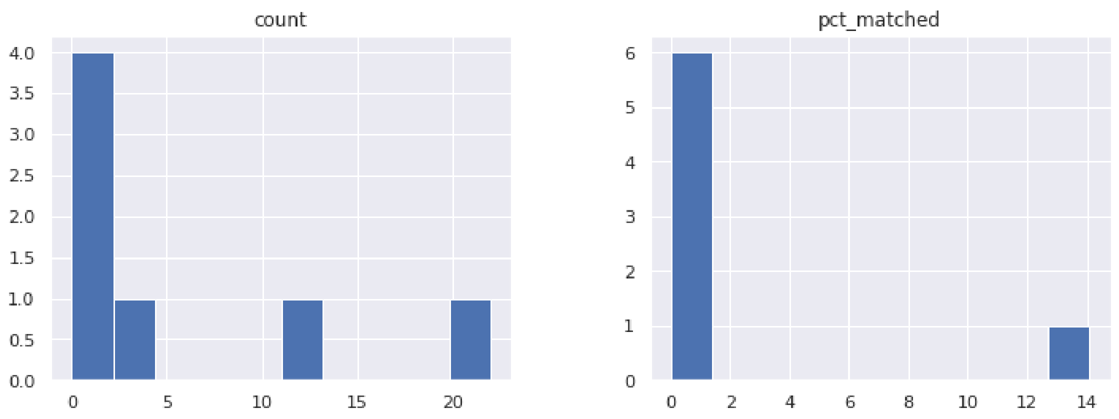
[31]:
```python
df=df_sra[df_sra['Name'].str.contains(s_name)]
```

[32]:
```python
df.drop(columns=['Name'],inplace=True)
sns.set(rc={"figure.figsize":(6, 6)})
df_box=df[['count', 'pct_matched']]
df_box.plot(kind='box', subplots=True, layout=(4,4), sharex=False,␣
 ↪sharey=False, figsize=(12,12))
```

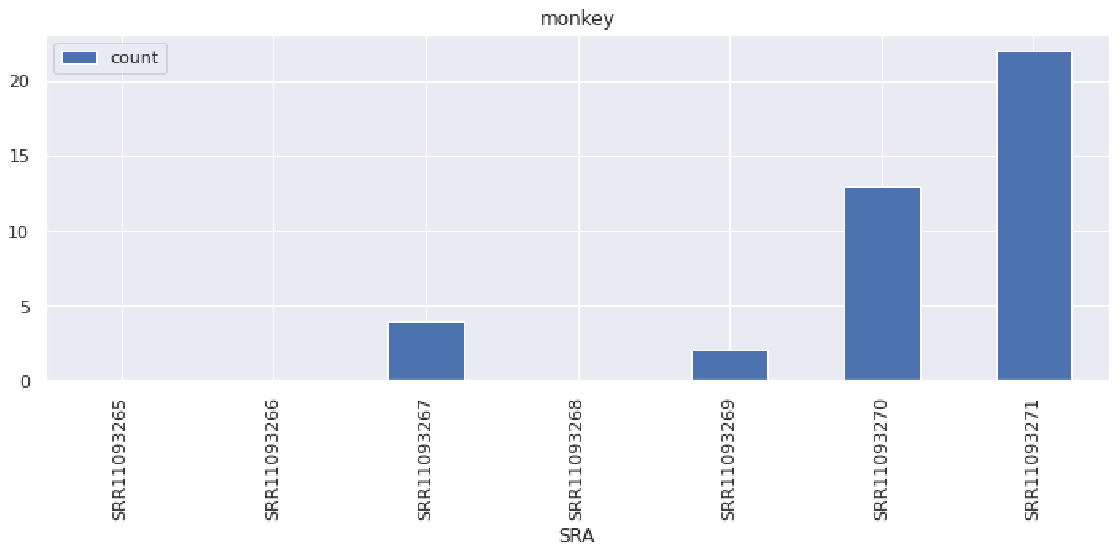
[32]:
```
count              AxesSubplot(0.125,0.71587;0.168478x0.16413)
pct_matched     AxesSubplot(0.327174,0.71587;0.168478x0.16413)
dtype: object
```



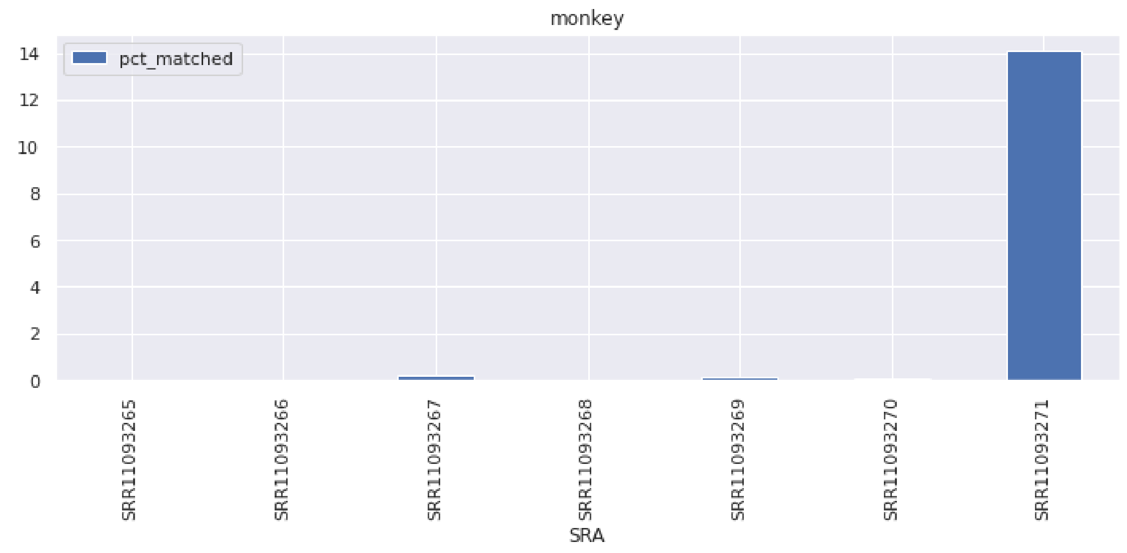
[33]:
```
df_box.hist(figsize=(12,4))
plt.show()
```



[34]:
```
ax=df.plot(x='SRA', y='count', kind='bar',figsize=(12,4))
ax.set_title(s_name, fontsize=12)
plt.show()
```



[35]:
```
ax=df.plot(x='SRA', y='pct_matched', kind='bar',figsize=(12,4))
ax.set_title(s_name, fontsize=12)
plt.show()
```



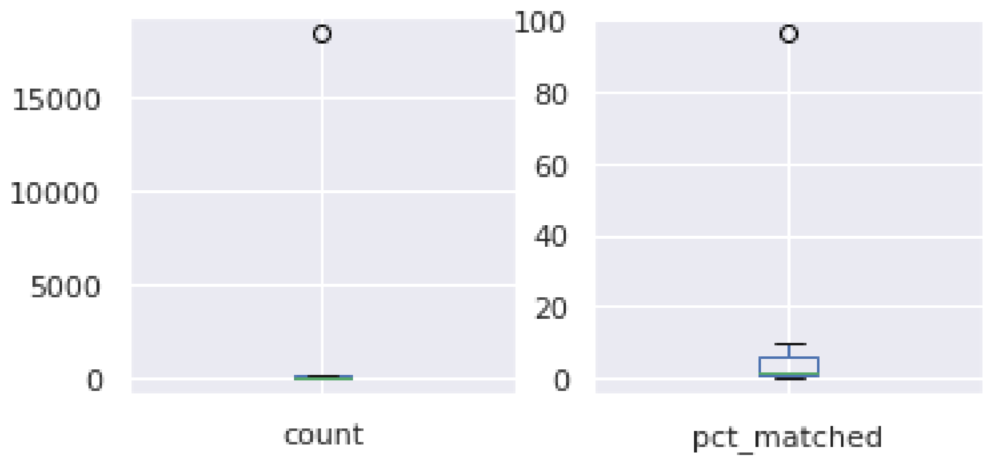
0.0.6 Pangolin

[36]:
```
s_name='pangolin'
```

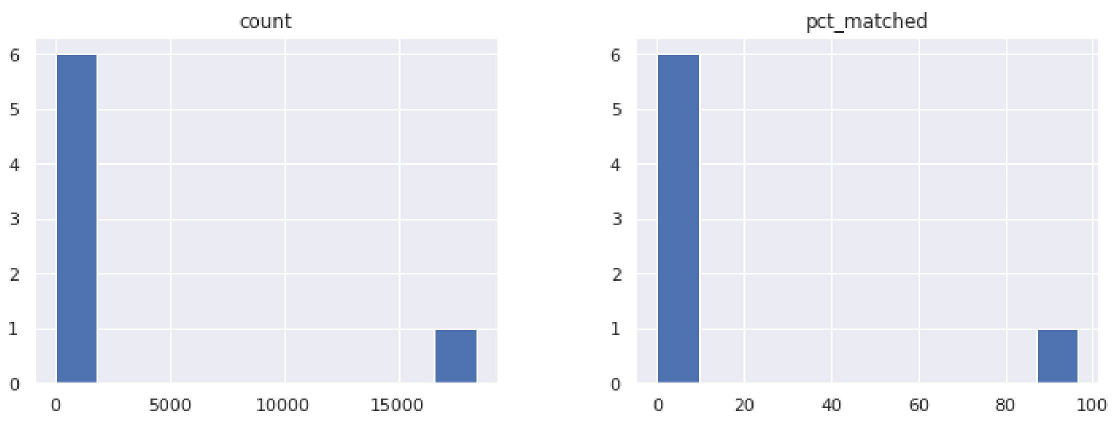
[37]:
```
df=df_sra[df_sra['Name'].str.contains(s_name)]
```

[38]:
```
df.drop(columns=['Name'],inplace=True)
sns.set(rc={"figure.figsize":(6, 6)})
df_box=df[['count', 'pct_matched']]
df_box.plot(kind='box', subplots=True, layout=(4,4), sharex=False,␣
 ↪sharey=False, figsize=(12,12))
```

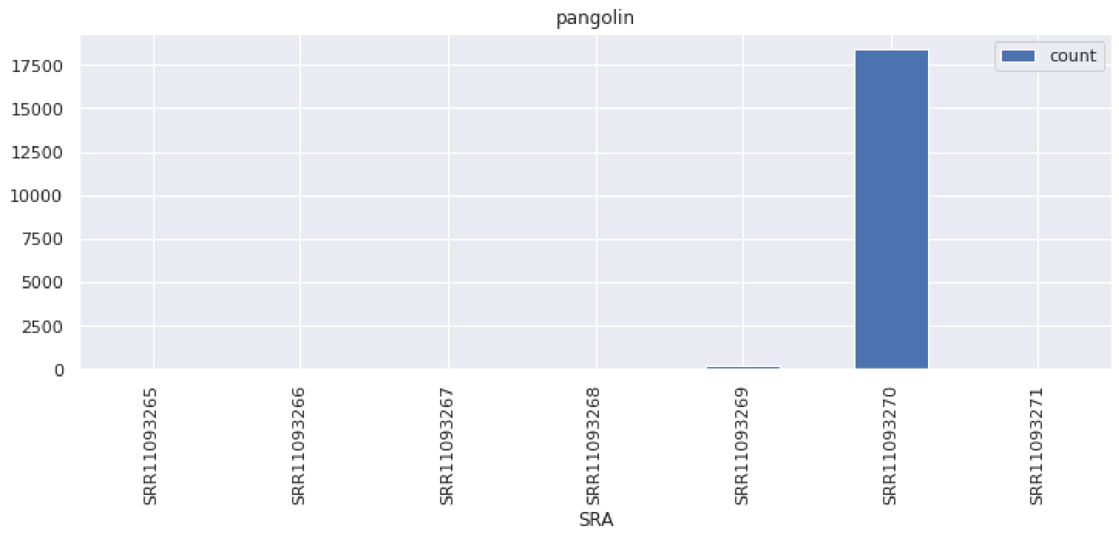
[38]:
```
count              AxesSubplot(0.125,0.71587;0.168478x0.16413)
pct_matched     AxesSubplot(0.327174,0.71587;0.168478x0.16413)
dtype: object
```



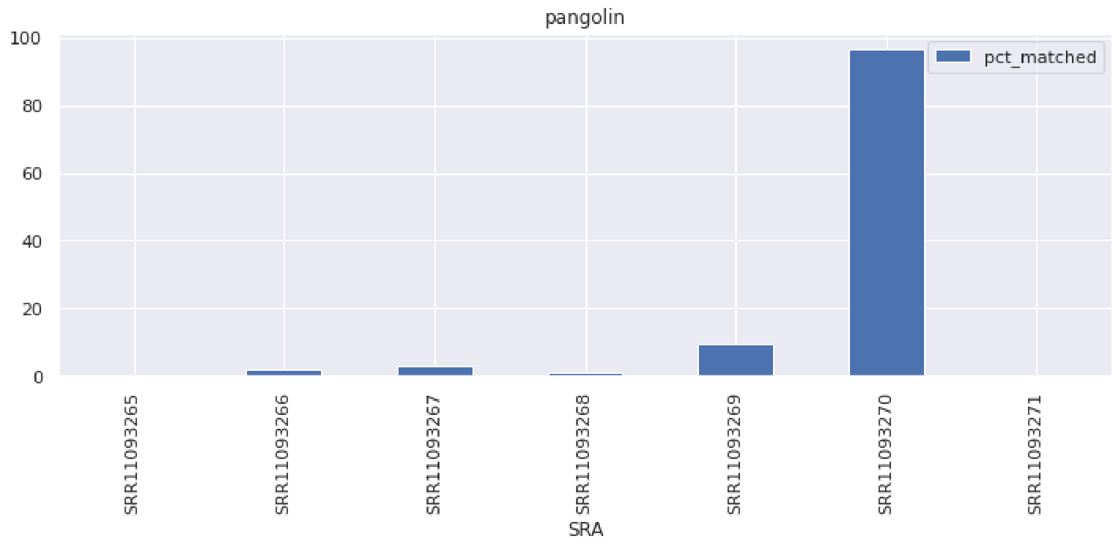
[39]:
```
df_box.hist(figsize=(12,4))
plt.show()
```



[40]:
```
ax=df.plot(x='SRA', y='count', kind='bar',figsize=(12,4))
ax.set_title(s_name, fontsize=12)
plt.show()
```



[41]:
```
ax=df.plot(x='SRA', y='pct_matched', kind='bar',figsize=(12,4))
ax.set_title(s_name, fontsize=12)
plt.show()
```



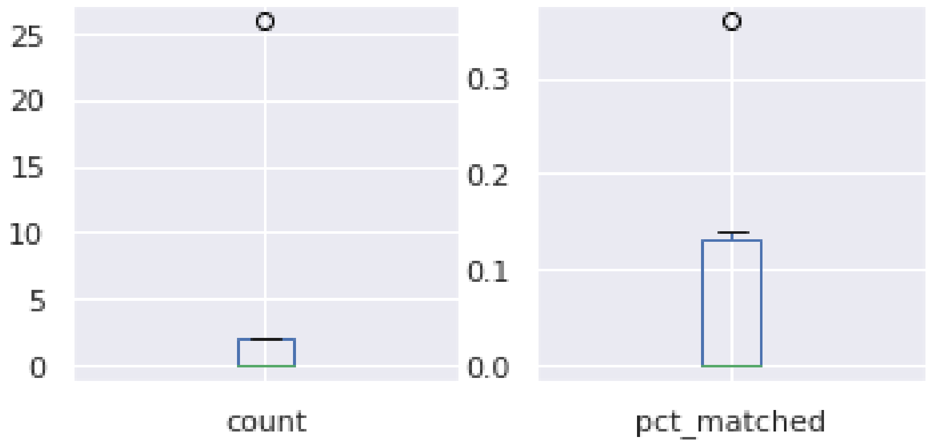
0.0.7 Mouse

[42]:
```
s_name='mouse'
```

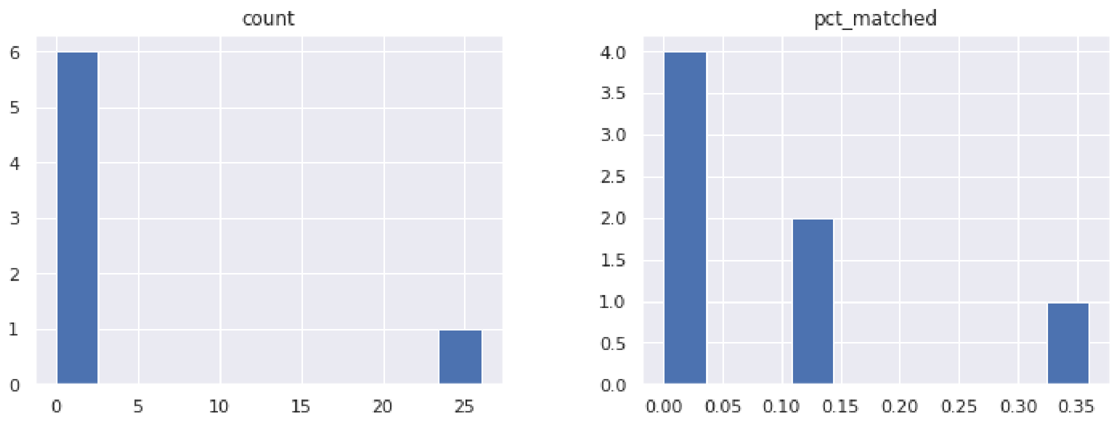
[43]:
```
df=df_sra[df_sra['Name'].str.contains(s_name)]
```

```
[44]: df.drop(columns=['Name'],inplace=True)
      sns.set(rc={"figure.figsize":(6, 6)})
      df_box=df[['count', 'pct_matched']]
      df_box.plot(kind='box', subplots=True, layout=(4,4), sharex=False,␣
       ↪sharey=False, figsize=(12,12))
```

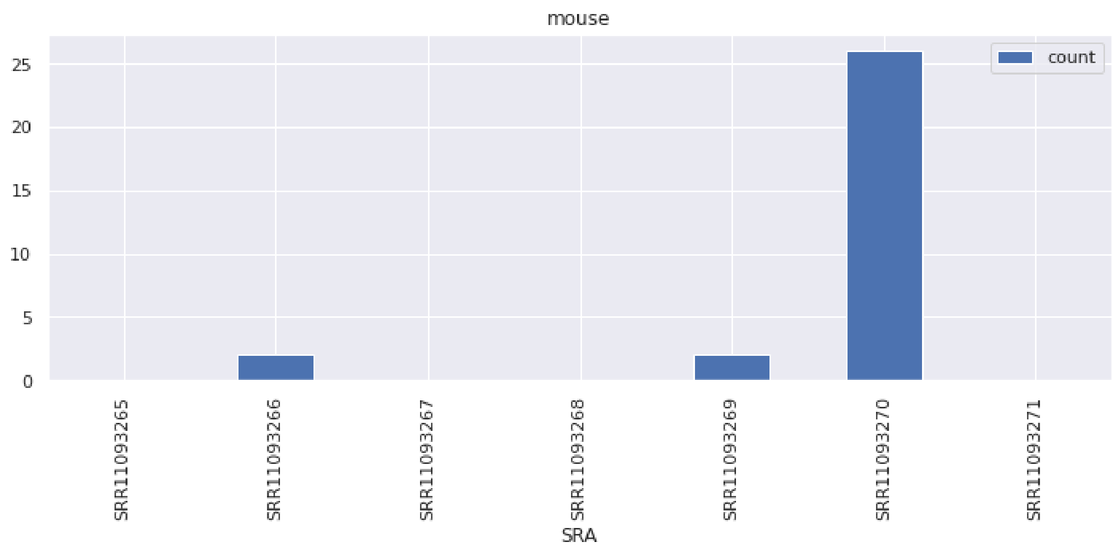
```
[44]: count                AxesSubplot(0.125,0.71587;0.168478x0.16413)
      pct_matched     AxesSubplot(0.327174,0.71587;0.168478x0.16413)
      dtype: object
```



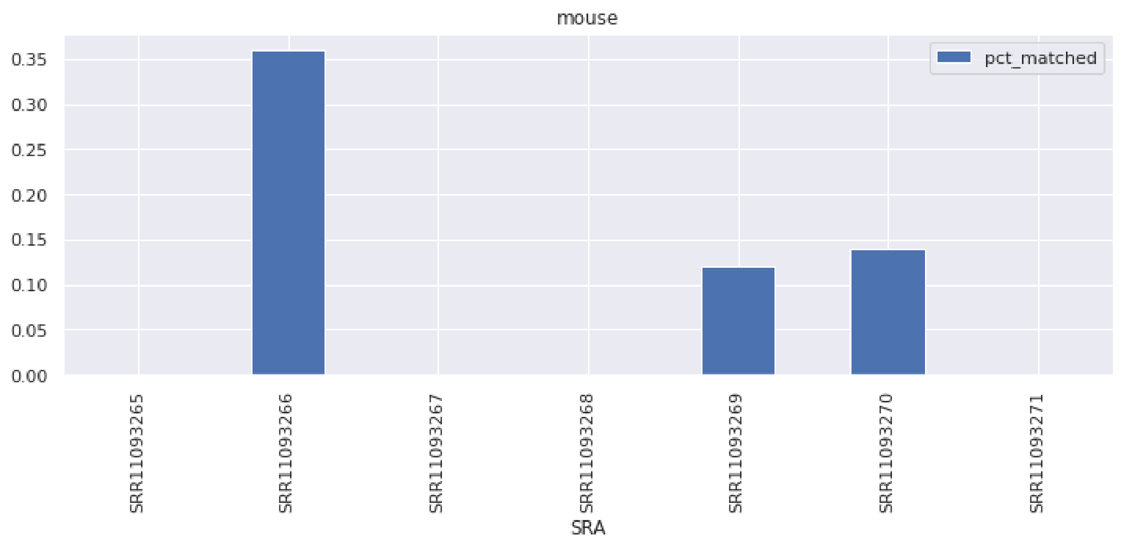
```
[45]: df_box.hist(figsize=(12,4))
      plt.show()
```



```
[46]: ax=df.plot(x='SRA', y='count', kind='bar',figsize=(12,4))
      ax.set_title(s_name, fontsize=12)
      plt.show()
```



[47]:
```
ax=df.plot(x='SRA', y='pct_matched', kind='bar',figsize=(12,4))
ax.set_title(s_name, fontsize=12)
plt.show()
```



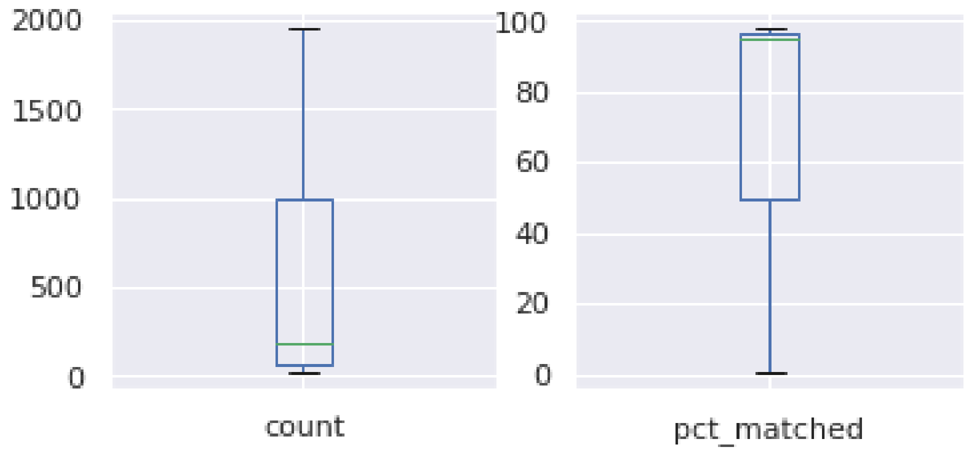
0.0.8 virus

[48]:
```
s_name='virus'
```

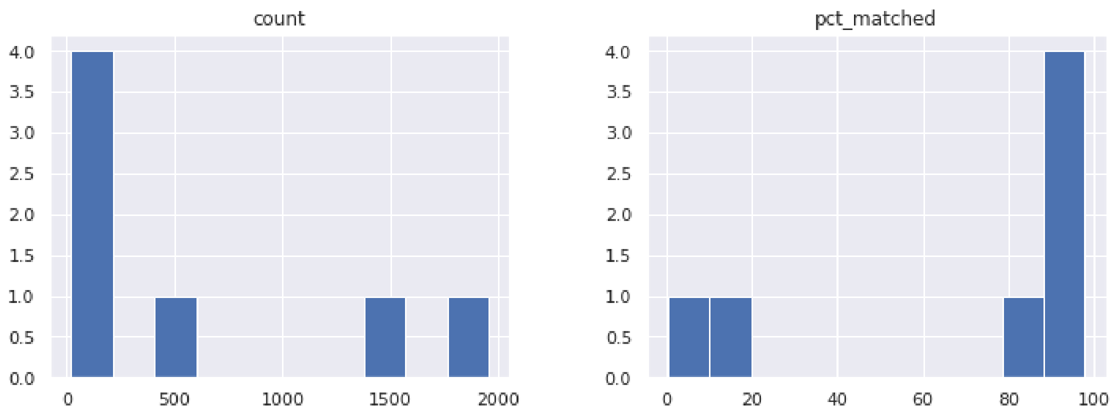
[49]:
```
df=df_sra[df_sra['Name'].str.contains(s_name)]
```

```
[50]: df.drop(columns=['Name'],inplace=True)
      sns.set(rc={"figure.figsize":(6, 6)})
      df_box=df[['count', 'pct_matched']]
      df_box.plot(kind='box', subplots=True, layout=(4,4), sharex=False,␣
       ↪sharey=False, figsize=(12,12))
```

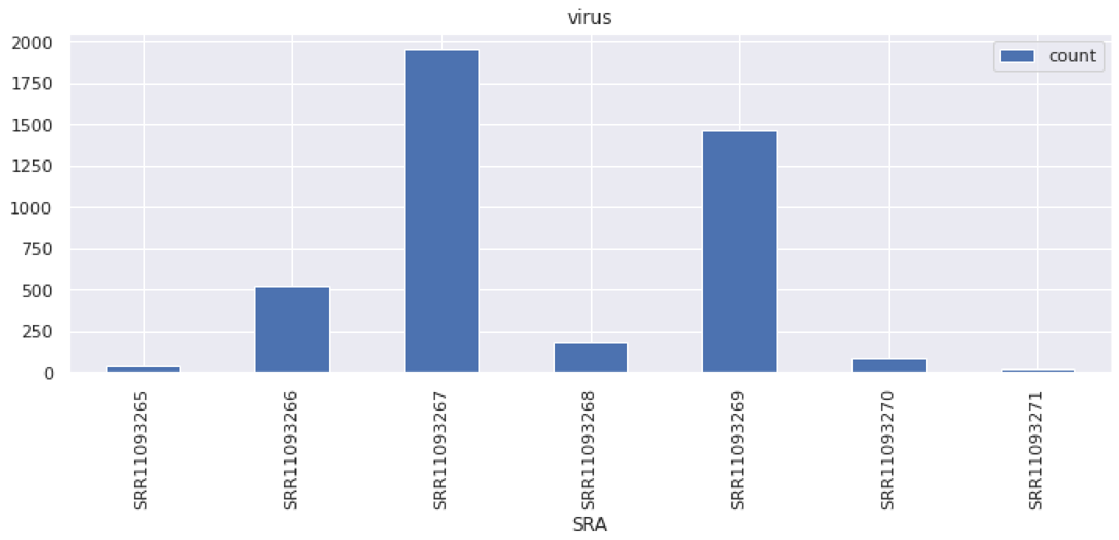
```
[50]: count              AxesSubplot(0.125,0.71587;0.168478x0.16413)
      pct_matched    AxesSubplot(0.327174,0.71587;0.168478x0.16413)
      dtype: object
```



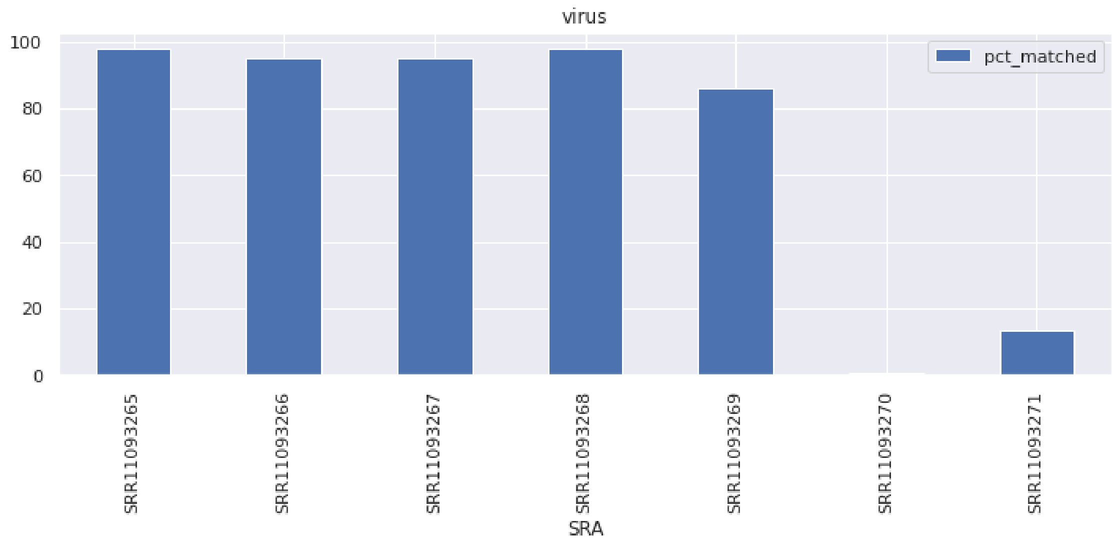
```
[51]: df_box.hist(figsize=(12,4))
      plt.show()
```



```
[52]: ax=df.plot(x='SRA', y='count', kind='bar',figsize=(12,4))
      ax.set_title(s_name, fontsize=12)
      plt.show()
```



[53]:
```
ax=df.plot(x='SRA', y='pct_matched', kind='bar',figsize=(12,4))
ax.set_title(s_name, fontsize=12)
plt.show()
```



0.0.9 Top nt database contigs matches per SRA

[54]:
```
def get_sra_dict(sra):
    total_dict={}
    asc_desc={}
    accessions, descriptions, counts, total=get_asc_descr_count(sra)
    for asc,desc,cnt in zip(accessions,descriptions, counts):
        if asc in total_dict:
            total_dict[asc]+=int(cnt)
        else:
            total_dict[asc]=int(cnt)
        if asc not in asc_desc:
            asc_desc[asc]=desc
    return total_dict, asc_desc, total
```

[55]:
```
for sra in sra_list:
    total_dict, asc_desc, total= get_sra_dict(sra)
    print(f'{sra}, number of contigs {total}')
    print_top_n_sp(total_dict, max_num=10)
    print('\n')
```

```
SRR11093265, number of contigs 10
Pangolin coronavirus isolate MP789, complete genome :  14
Pangolin coronavirus isolate MP789 genomic sequence :  10
Pangolin coronavirus isolate cDNA8-S surface glycoprotein (S) gene, complete cds
:  3
Pangolin coronavirus isolate cDNA9-S surface glycoprotein (S) gene, complete cds
:  3
Pangolin coronavirus isolate cDNA16-S surface glycoprotein (S) gene, complete
cds :  3
Pangolin coronavirus isolate cDNA18-S surface glycoprotein (S) gene, complete
cds :  3
Pangolin coronavirus isolate cDNA20-S surface glycoprotein (S) gene, complete
cds :  3
Pangolin coronavirus isolate cDNA31-S surface glycoprotein (S) gene, complete
cds :  3
Severe acute respiratory syndrome coronavirus 2 isolate 230077 genome assembly,
chromosome: 1 :  1
Synthetic construct clone C35/41, complete sequence :  1


SRR11093266, number of contigs 34
Pangolin coronavirus isolate PCoV_GX-P1E, complete genome :  117
Pangolin coronavirus isolate PCoV_GX-P2V, complete genome :  95
Pangolin coronavirus isolate PCoV_GX-P4L, complete genome :  90
Pangolin coronavirus isolate PCoV_GX-P5L, complete genome :  74
Pangolin coronavirus isolate PCoV_GX-P5E, complete genome :  72
Pangolin coronavirus isolate PCoV_GX-P3B genomic sequence :  72
Lutra lutra genome assembly, chromosome: 16 :  2
Manis javanica isolate MP_PG03-UM mitochondrion, complete genome :  1
Mus musculus clone contig 1 chromocenter region genomic sequence :  1
Mus musculus clone contig 5 chromocenter region genomic sequence :  1
```

```
SRR11093267, number of contigs 100
Pangolin coronavirus isolate PCoV_GX-P5L, complete genome :  449
Pangolin coronavirus isolate PCoV_GX-P1E, complete genome :  366
Pangolin coronavirus isolate PCoV_GX-P2V, complete genome :  347
Pangolin coronavirus isolate PCoV_GX-P5E, complete genome :  338
Pangolin coronavirus isolate PCoV_GX-P4L, complete genome :  326
Pangolin coronavirus isolate PCoV_GX-P3B genomic sequence :  126
PREDICTED: Manis pentadactyla uncharacterized LOC118928956 (LOC118928956), ncRNA
:  3
Manis javanica isolate MP_PG03-UM mitochondrion, complete genome :  2
Manis javanica isolate EP2 mitochondrion, complete genome :  2
Canis lupus familiaris breed Labrador retriever chromosome 30b :  2


SRR11093268, number of contigs 10
Pangolin coronavirus isolate PCoV_GX-P5E, complete genome :  43
Pangolin coronavirus isolate PCoV_GX-P5L, complete genome :  40
Pangolin coronavirus isolate PCoV_GX-P2V, complete genome :  37
Pangolin coronavirus isolate PCoV_GX-P1E, complete genome :  31
Pangolin coronavirus isolate PCoV_GX-P4L, complete genome :  23
Pangolin coronavirus isolate PCoV_GX-P3B genomic sequence :  11
Lutra lutra genome assembly, chromosome: 16 :  1
PREDICTED: Manis javanica phosphatidylinositol glycan anchor biosynthesis class
Q (PIGQ), transcript variant X7, mRNA :  1
PREDICTED: Manis javanica uncharacterized LOC118969509 (LOC118969509), ncRNA :
1
PREDICTED: Canis lupus familiaris collagen alpha-1(I) chain-like (LOC119879328),
misc_RNA :  1


SRR11093269, number of contigs 223
Pangolin coronavirus isolate PCoV_GX-P4L, complete genome :  261
Pangolin coronavirus isolate PCoV_GX-P5L, complete genome :  259
Pangolin coronavirus isolate PCoV_GX-P1E, complete genome :  257
Pangolin coronavirus isolate PCoV_GX-P2V, complete genome :  255
Pangolin coronavirus isolate PCoV_GX-P3B genomic sequence :  253
Pangolin coronavirus isolate PCoV_GX-P5E, complete genome :  173
Megaerops niphanae clone Mnip32b LINE-1 retroposon ORF II pseudogene, partial
sequence :  5
Manis tricuspis clone Mtri123b LINE-1 retroposon ORF II pseudogene, partial
sequence :  4
Manis tricuspis clone Mtri131b LINE-1 retroposon ORF II pseudogene, partial
sequence :  3
Canis lupus familiaris breed Labrador retriever chromosome 30b :  2


SRR11093270, number of contigs 11832
```

```
Pangolin coronavirus isolate PCoV_GX-P3B genomic sequence :  16
PREDICTED: Manis javanica proline rich coiled-coil 2A (PRRC2A), mRNA :  15
Pangolin coronavirus isolate PCoV_GX-P1E, complete genome :  14
PREDICTED: Manis javanica LDL receptor related protein 1 (LRP1), transcript
variant X3, mRNA :  14
PREDICTED: Manis javanica LDL receptor related protein 1 (LRP1), transcript
variant X4, mRNA :  14
Pangolin coronavirus isolate PCoV_GX-P4L, complete genome :  13
PREDICTED: Manis javanica LDL receptor related protein 1 (LRP1), transcript
variant X1, mRNA :  13
PREDICTED: Manis javanica LDL receptor related protein 1 (LRP1), transcript
variant X2, mRNA :  13
Erysipelothrix rhusiopathiae strain KC-Sb-R1 chromosome, complete genome :  12
Pangolin coronavirus isolate PCoV_GX-P5L, complete genome :  12


SRR11093271, number of contigs 74
Pangolin coronavirus isolate PCoV_GX-P2V, complete genome :  11
Mycoplasma arginini strain HAZ145_1 :  10
Mycoplasma arginini strain NCTC10129 chromosome 1 :  8
Mycoplasma hyorhinis strain NCTC10130 genome assembly, chromosome: 1 :  4
Mycoplasma hyorhinis strain NCTC10121 genome assembly, plasmid: 3 :  4
Mycoplasma hyorhinis strain JF5820 chromosome, complete genome :  4
Mycoplasma hyorhinis strain IMT49388 chromosome, complete genome :  4
Mycoplasma hyorhinis HUB-1, complete genome :  4
Mycoplasma hyorhinis GDL-1, complete genome :  4
Mycoplasma hyorhinis SK76, complete genome :  4
```

[56]:
```
### Get specific contigs matching a species/name
```

[57]:
```
def write_contigs(sra, match_names):
    accessions, descriptions, counts, total=get_asc_descr_count(sra)
    asc_matches=[]
    for m in match_names:
        for a,d in zip(accessions, descriptions):
            if m.lower() in d.lower():
                asc_matches.append(a)
    gi_matches=[]
    for a in asc_matches:
        idx=ACCESSIONS.index(a)
        gi=GIS[idx]
        gi_matches.append(gi)
    contigs=[]
    path = BASE_PATH+sra+'/magic_blast/'
    subset_f = open(path+f'{sra}_{match_names[0].replace(" ",␣
↪"_")}_subset_{f_contigs_file_tail}', 'w')
    with open(path+f'{sra}{f_contigs_file_tail}', 'r') as f:
        lines = [line for line in f]
        for line in lines:
            for gi in gi_matches:
                if gi in line:
                    parts=line.split('\t')
                    idx=GIS.index(gi)
                    asc=ACCESSIONS[idx]
                    t=TITLES[idx]
                    ps=parts[:2]
                    pe=parts[3:]
                    ps.append(asc+' '+t.rstrip('\n'))
                    parts=ps+pe
                    p='\t'.join(parts)
                    subset_f.write(p)
    subset_f.close()
```

[ ]:

```
[58]: set_accessions() #time consuming, comment out if already ran
assert ACCESSIONS is not None
```

```
[59]: #match_names=['vector']
#for sra in sra_list:
#    write_contigs(sra, match_names)
```

```
[60]: #match_names=['plasmid']
#for sra in sra_list:
#    write_contigs(sra, match_names)
```

```
[61]: #match_names=['mustela']
#for sra in sra_list:
#    write_contigs(sra, match_names)
```

```
[ ]: match_names=['virus']
for sra in sra_list:
    write_contigs(sra, match_names)
```

[ ]: